Test-Kit Intervention Strategy for COVID-19 using Dynamic Networks

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I. Introduction

In recent years, humanity has been affected by several infectious diseases. Thus, the study and analysis of diseases and how they spread has garnered significant interest. This has led to the rise of the field of epidemiology, and,in turn, the development of mathematical models for diseases. These includes modeling approach such as *compartmental models*. In compartmental models, the population of interest is divided into compartments of interest and the dynamics of the members of the group between the compartments is modelled using mathematical equations.

II. Compartmental Models

In this section, we will go through a few examples of well-studied compartmental models used in Epidemiology.

A. The SIR Model

One of the earliest works in the compartmentalised study of infectious diseases was done by Kermack & McKendrick in 1927 [1]. They divided the population into three compartments, namely *Susceptible* (S), *Infected* (I) and *Removed* (R). The SIR model is one of the simplest compartmental models. the dynamic equations for the SIR model is as given below:

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta IS}{N},\\ \frac{dI}{dt} &= \frac{\beta IS}{N} - \gamma I,\\ \frac{dR}{dt} &= \gamma I,\end{aligned}$$

where $S+I+R=1$, since each compartment represents a fraction of population. These equations are diagrammatically represented in 1.

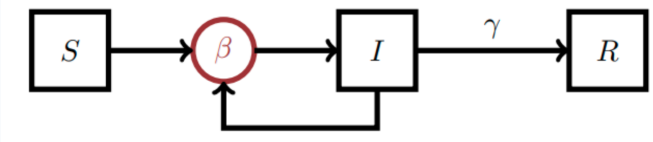


Fig. 1: Diagrammatic Representation of the SIR Model

B. The SEIR Model

Several epidemiology models have been since proposed, many of which are modifications of the SIR model. One such model is the SEIR model [2]. In this framework, the population is split into four compartments, namely *Susceptible* (S), *Exposed* (E), *Infected* (I) and *Removed* (R). The dynamic equations for the same are as given:

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta IS}{N},\\ \frac{dE}{dt} &= \frac{\beta IS}{N} - \sigma E,\\ \frac{dI}{dt} &= \sigma E - \gamma I,\\ \frac{dR}{dt} &= \gamma I,\end{aligned}$$

where $S+E+I+R=1$, since each compartment represents a fraction of population. These equations are diagrammatically represented in 2.

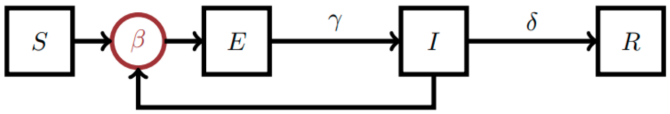


Fig. 2: Diagrammatic Representation of the SEIR Model

C. The SAIR Model

Some diseases, in particular viral disease, go through an incubation phase. During this phase, the person is asymptotic, but can spread the disease to others. Several other disease also show asymptotic carriers, who themselves are not affected, but can transmit the disease.

The SAIR model [3], [4] aims to encapsulate this phenomenon. In this model, the Exposed (E) category is replaced with *Asymptotic* (A). A newly infected person initially enters the Asymptotic group from Susceptible group, before entering the Infected or Removed groups. The dynamic equations for the same are as given:

$$\frac{dS}{dt} = -\beta_A AS - \beta_I IS,$$
$$\frac{dA}{dt} = \beta_A AS + \beta_I IS - \gamma_A A - \delta A,$$
$$\frac{dI}{dt} = \delta A - \gamma_I I,$$
$$\frac{dR}{dt} = \gamma_A A + \gamma_I I,$$

where $S+A+I+R = 1$, since each compartment represents a fraction of population. These equations are diagrammatically represented in 3.

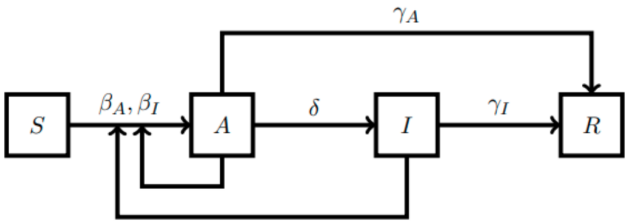


Fig. 3: Diagrammatic Representation of the SEIR Model

D. The SUTRA Model

SUTRA stands for ***S**usceptible, **U**ndected, **T**ested Positve, **R**emoved **A**pproach*. The authors of this paper, claim that this approach more realistic model, as it does not consider asymptotic and infected categories as separate. Instead, this approach replaces these groups with *Undetected* (U) and *Tested Positive* (T). The dynamcis of the model are as given below;

$$\frac{dS}{dt} = -\beta SU,$$
$$\frac{dU}{dt} = \beta SU - \epsilon\beta SU - \gamma U,$$
$$\frac{dT}{dt} = \epsilon\beta SU - \gamma T,$$
$$\frac{dR}{dt} = \gamma U + \gamma T,$$

where $S+U+T+R = 1$, since each compartment represents a fraction of population. These equations are diagrammatically represented in 4.

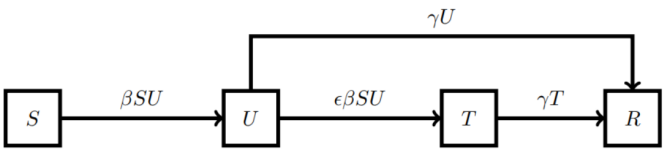


Fig. 4: Diagrammatic Representation of the SEIR Model

on of population. These equations are diagrammatically represented in 4.

SUTRA model claimed to be a "super-model" capable of modeling and predicting the COVID-19 pandemic. However, drew a lot of controversy when it failed to predict the second wave in India. Further, the model depends on parameters that were found by linear regression on the daily data. Then these parameters were fit into the equations to regain the daily data again. This method, thus, is very questionable and seems rather *a posteriori*.

E. Work Done by Us During this Semester

Through the course of the semester, we worked on the aforementioned epidemiology models.

In our first paper presentation, we had presented the SUTRA model. We had also recreated the graphs for the number of people tested positive, for both South Korea and India, using the model. However, due to the issues mentioned earlier, we decided to not continue working on this model.

For our second paper presentation, we took up the paper "Optimal test-kit-based intervention strategy of epidemic spreading in heterogeneous complex networks" (Ghosh et al, 2021) [5]. This paper showed that test-kit based intervention can reduce the final outbreak size and the peak of infection.

For our presentation, we reproduced the simulation results shown in the initial part of [5]. We obtained the graphs for each of the population compartments, the values of final outbreak size (Z_{FOS}) and the peak of infection (I_{max}), the presence and absence of test-kits. This was done considering the population to be one group, without involving the network approach employed in the later part of the paper.

For our final presentation, we have continued along the lines of the network approach from the [5].

III. Test-Kit Based Intervention Strategy

As mentioned earlier, [5] showed the impact of test-kit based intervention strategies in mitigating pandemics.

A. Single-Node Model Description

For the entire population (single-node) case, the paper used a modified version of the SEIR Model. It considered 5 categories, namely *Susceptible* (S), *Exposed* (E), *Infected* (I) and *Removed* (R), corresponding to the SEIR model, and an additional category for *Hospitalised* (H). *The number of test-kits* is given by the variable K. The dynamic equations for this model are as given below:

$$\frac{dS}{dt} = -\frac{\beta SI}{N},$$
$$\frac{dE}{dt} = \frac{\beta IS}{N} - \sigma E,$$
$$\frac{dI}{dt} = \sigma E - \alpha(K)I,$$
$$\frac{dH}{dt} = \alpha(K)I - \gamma H,$$
$$\frac{dR}{dt} = \gamma H,$$
$$\frac{dK}{dt} = \xi I - \chi K,$$

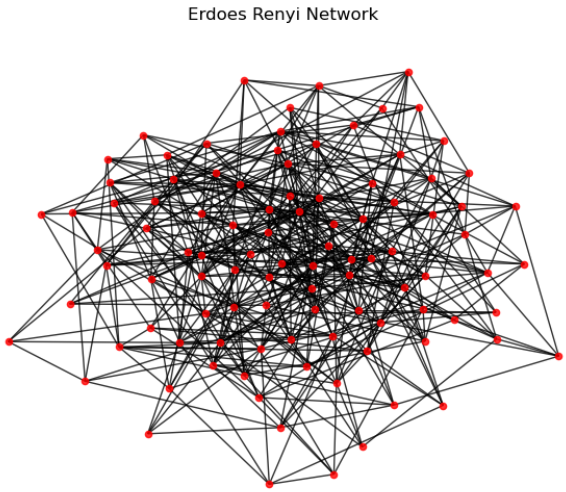


Fig. 5: Erdős–Rényi Network Visualisation

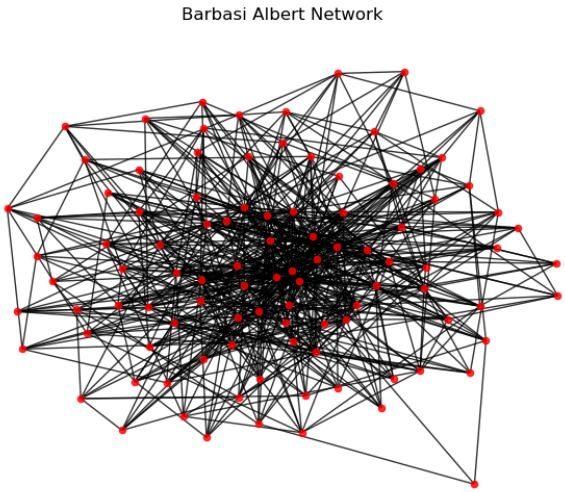


Fig. 6: Barabási–Albert Network Visualisation

where $S + E + I + H + R = 1$, since each compartment represents a fraction of population. Here, $\alpha(K)$ is controls the rate of hospitalisation and is given as:

$$\alpha(K) = \alpha_0 + \alpha_1 K.$$

where α_0 accounts for hospitalisations due to appearance of symptoms, irrespective of test-kits. Further, ξ controls the production rate of test-kits.

B. Meta-Population Network

The above approach is extended to a meta-population network. The authors consider the population to be a network of M patches or nodes, with the n^{the} node having N_n total population that is susceptible. The dynamic equations for such a case is given as:

$$\frac{dS_n}{dt} = -\frac{\beta_n S_n I_n}{N_n} + \frac{\epsilon}{d_n}\sum_{m=1}^{M} A_{nm}(S_m - S_n),$$

$$\frac{dE_n}{dt} = \frac{\beta_n I_n S_n}{N_n} - \sigma E_n + \frac{\epsilon}{d_n}\sum_{m=1}^{M} A_{nm}(E_m - E_n),$$

$$\frac{dI_n}{dt} = \sigma E_n - (\alpha_0 + g_n(K))I_n + \frac{\epsilon}{d_n}\sum_{m=1}^{M} A_{nm}(I_m - I_n),$$

$$\frac{dH_n}{dt} = (\alpha_0 + g_n(K))I_n - \gamma H_n,$$

$$\frac{dR_n}{dt} = \gamma H_n + \frac{\epsilon}{d_n}\sum_{m=1}^{M} A_{nm}(R_m - R_n),$$

$$\frac{dK}{dt} = \xi \sum_{n=1}^{M} I_n - \chi K$$

C. Intervention Strategies

Five different intervention strategies are considered for studying the impact of testkits on the dynamics of the pandemic. They are:

1) Degree centrality based test-kit Strategy (SD): The testkits are distributed and divided according to the degree of the patches of the network.

2) Identically-Distributed test-kit Strategy (SI): The testkits are distributed and divided according to the degree of the patches of the network.

3) Betweeness-Centrality based Strategy (SB): Patches with high betweeness centrality values are chosen and the testkits are distributed among them according to their magnitudes.

4) Local-Clustering based Strategy (SC): Patches with high local clustering coefficients are chosen and the testkits are distributed among them according to their magnitudes.

5) Strategy without Testkits (SW): This intervention strategy does not consider any testkits.

Figures 8 and 7 show the nodes selected by the above mentioned intervention strategies with p = 0.1 i.e. 10 nodes are selected out of the total 100 nodes in the network.

IV. Results

We performed the simulation of the dynamics described by the equations above on both Erdős–Rényi Networks (Number of Nodes (n) = 100, Edge Probability = 0.1) 5 and Barabási–Albert (Scale-Free) Networks (Number of Nodes (n) = 100, Average Degree ($< d >$) = 6) 6. We also obtained peak infection value I_{max} and the final outbreak size Z_{FOS}, across different values of p and ϵ. Here p is the percentage of nodes which are considered while distributing the test-kits. The variable p corresponds to the variable N_d in [5]. The results are discussed in detail in the following subsections.

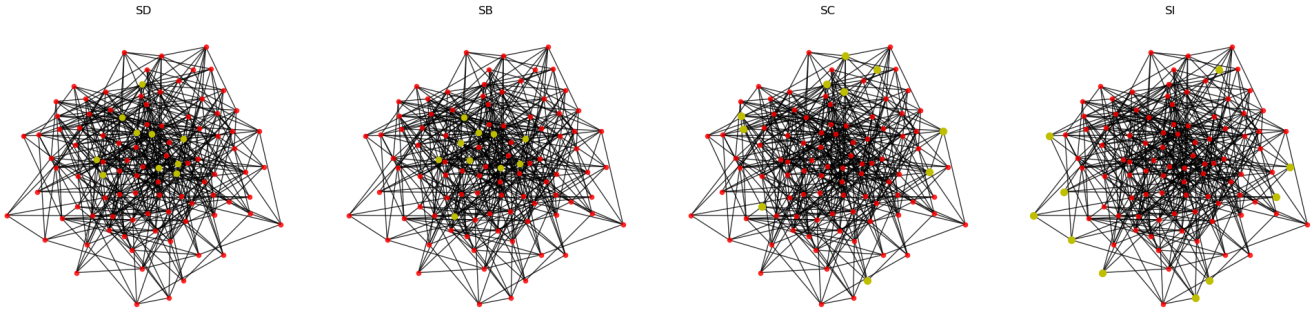


Fig. 7: Intervention strategies on Erdős–Rényi Network Visualisation

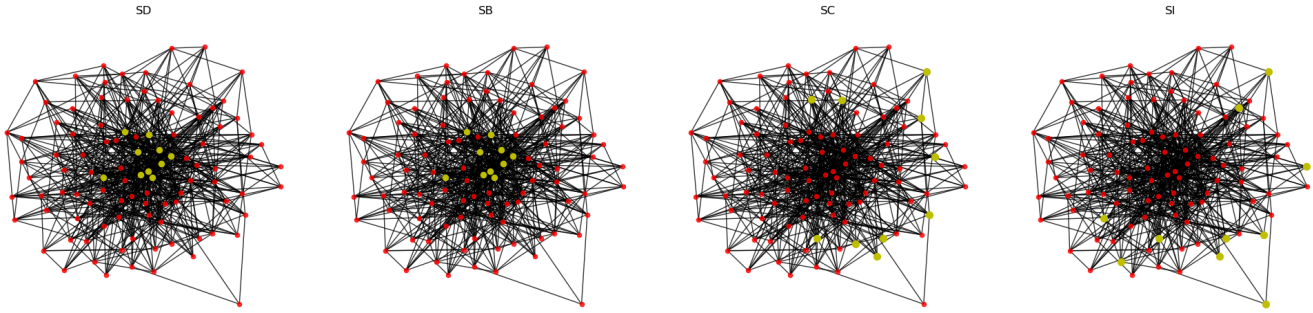


Fig. 8: Intervention strategies on Barabási–Albert Network

A. *Effect of I_{max} on varying p and ϵ*

From Figures 9 and 10, there are multiple observations on I_{max} that can be made on varying ϵ and n:

- On increasing ϵ values from 0.005 to 0.5, for a given value of N_d, I_{max} reduces.
- SB and SD have more pronounced reduction trend in I_{max} values in Erdos-Renyi compared to Barabasi-Albert Network.
- SC and SI have more pronounced reduction trend in I_{max} values in Barabasi-Albert compared to Erdos-Renyi Network.
- For small ϵ values, I_{max} shows a steady decrease as p increases.
- However for larger ϵ values, graph behaves differently, with the I_{max} values for SB and SD showing an increasing trend with respect to increasing p.
- There seems to be a high degree of synchronisation, in case of higher values of ϵ.

B. *Effect of Z_{FOS} on varying p and ϵ*

From Figures 11 and 12, there are multiple observations on Z_{FOS} that can be made on varying ϵ and n:

- On increasing ϵ values from 0.005 to 0.5, for a given value of N_d, Z_{FOS} reduces.
- SB and SD have more pronounced reduction trend in Z_{FOS} values in Erdos-Renyi compared to Barabasi-Albert Network.
- SC and SI have more pronounced reduction trend in Z_{FOS} values in Barabasi-Albert compared to Erdos-Renyi Network.
- For small ϵ values, I_{max} shows a steady decrease as p increases.
- However for larger ϵ values, graph behaves differently, with the Z_{FOS} values for SB and SD showing an increasing trend with respect to increasing p.
- There seems to be a high degree of synchronisation, in case of higher values of ϵ.

C. *Analysis of Second Wave*

The values in each node was plotted and analysed for both cases. However, neither case indicated the occurrence of a second wave.

V. Conclusion

The dynamics of disease spreading on both Erdős–Rényi Networks and Barabási–Albert (Scale-Free) Networks was simulated and analysed by us, using the dynamic equations mentioned in [5]. The variation of the I_{max} and Z_{FOS} with respect to p, across different ϵ values were considered and analysed.

References

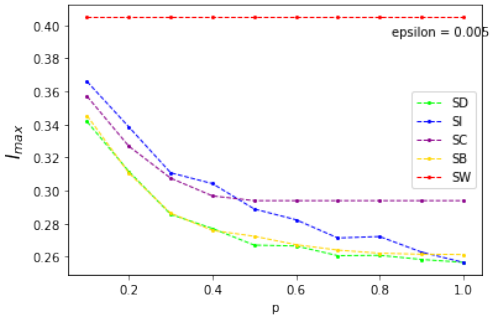
[1] W. O. Kermack and A. G. McKendrick, "A contribution to the mathematical theory of epidemics," *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*, vol. 115, no. 772, pp. 700–721, 1927.

[2] S. Mwalili, M. Kimathi, V. Ojiambo, D. Gathungu, and R. Mbogo, "Seir model for covid-19 dynamics incorporating the environment and social distancing," *BMC Research Notes*, vol. 13, 12 2020.

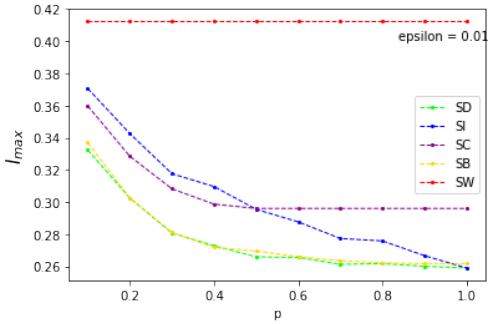
[3] M. Robinson and N. I. Stilianakis, "A model for the emergence of drug resistance in the presence of asymptomatic infections," *Mathematical Biosciences*, vol. 243, no. 2, pp. 163–177, 2013.

[4] S. Ansumali, S. Kaushal, A. Kumar, M. K. Prakash, and M. Vidyasagar, "Modelling a pandemic with asymptomatic patients, impact of lockdown and herd immunity, with applications to sars-cov-2," *Annual Reviews in Control*, vol. 50, pp. 432–447, 2020.

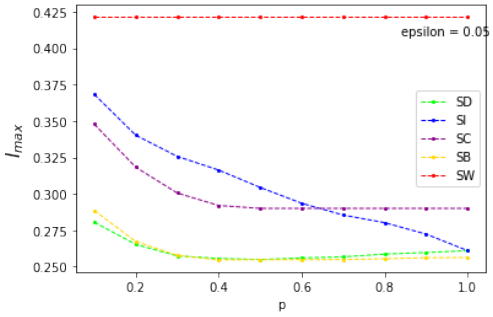
[5] S. Ghosh, A. Senapati, J. Chattopadhyay, C. Hens, and D. Ghosh, "Optimal test-kit-based intervention strategy of epidemic spreading in heterogeneous complex networks," *Chaos: An Interdisciplinary Journal of Nonlinear Science*, vol. 31, no. 7, p. 071101, 2021.



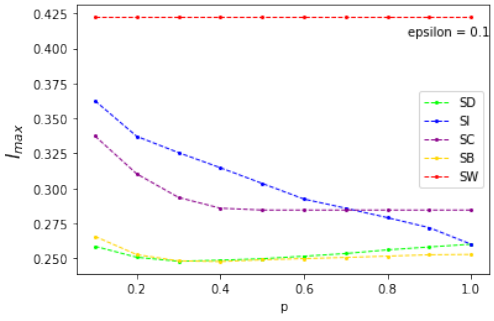
(a) ϵ = 0.005



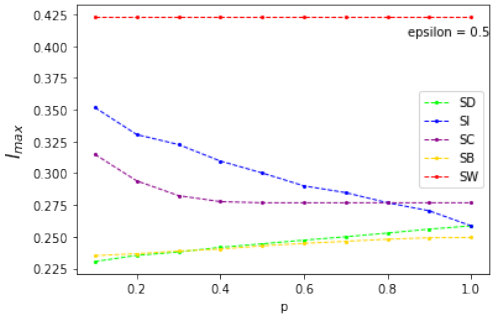
(b) ϵ = 0.01



(c) ϵ = 0.05

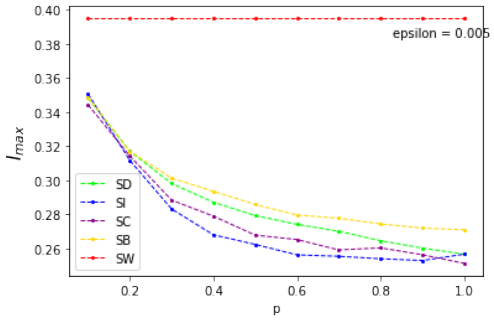


(d) ϵ = 0.1



(e) ϵ = 0.5

Fig. 9: Plots of I_{max} vs % nodes considered for testkits distribution in a Erdos Renyi Network for N = 100



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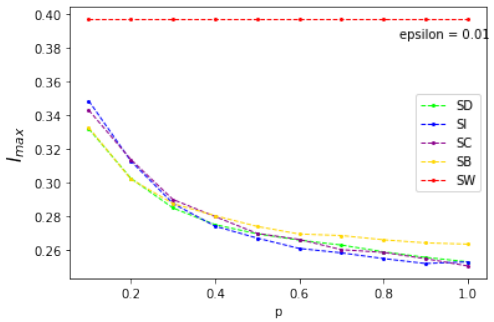
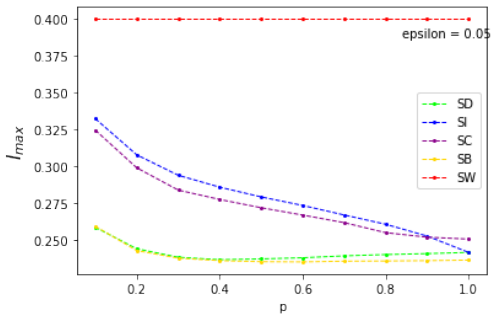
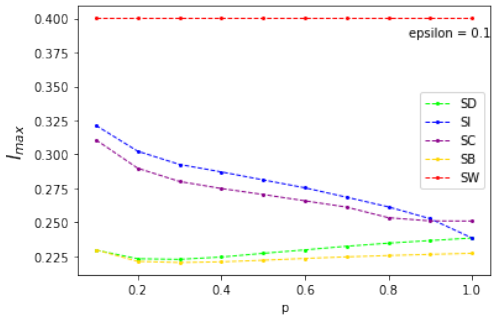


(b) ϵ = 0.01



(c) ϵ = 0.05



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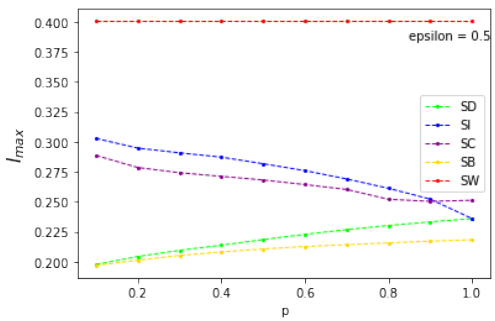
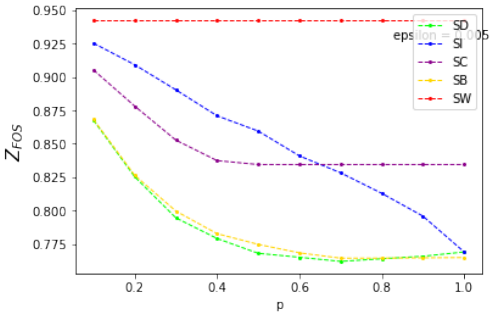
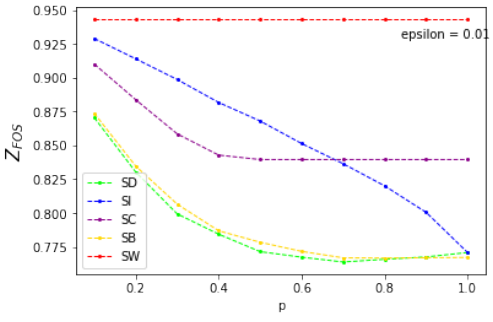


(e) ϵ = 0.5

Fig. 10: Plots of I_{max} vs % nodes considered for testkits distribution in a Scale-Free Network for N = 100



(a) ϵ = 0.005



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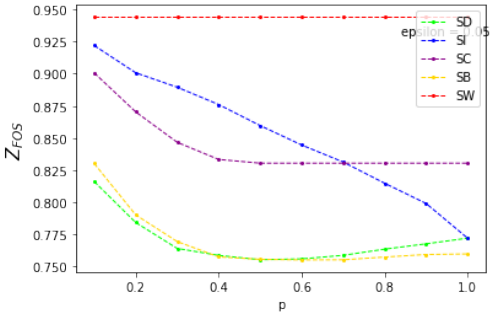

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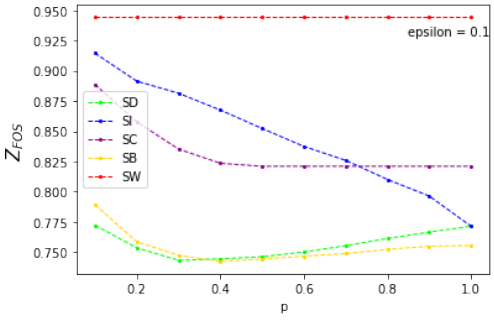

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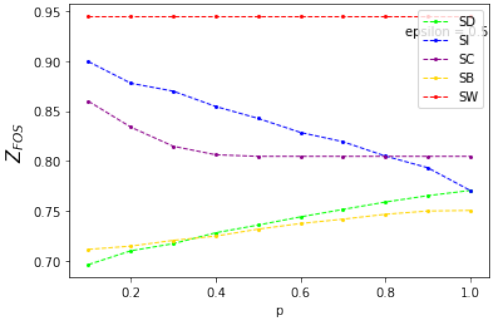
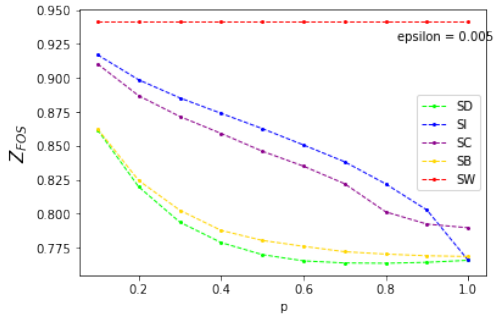
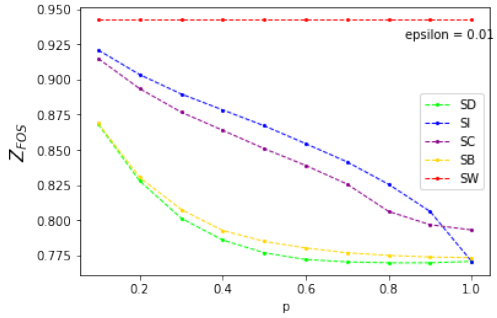


(e) ϵ = 0.5

Fig. 11: Plots of Z_{FOS} vs % nodes considered for testkits distribution in a Erdos-Renyi Network for N = 100



(a) ϵ = 0.005



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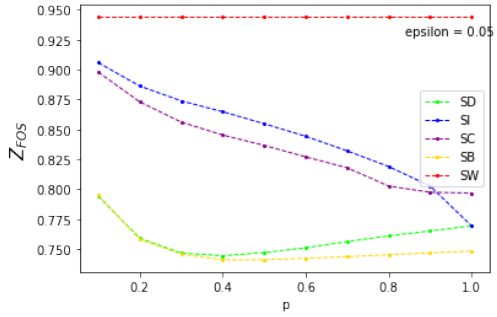

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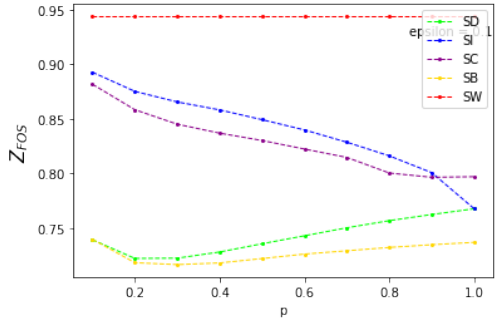
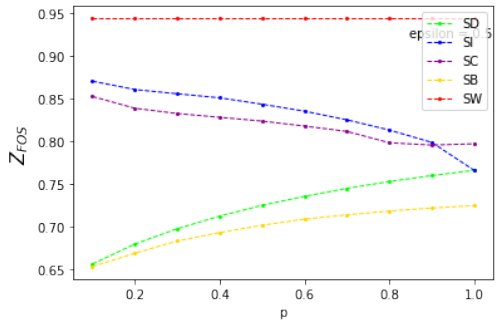


(d) ϵ = 0.1



(e) ϵ = 0.5

Fig. 12: Plots of Z_{FOS} vs % nodes considered for testkits distribution in a Scale-Free Network for N = 100